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> d his

     (FILE 'HOME' ENTERED AT 16:42:35 ON 21 JAN 96)

     FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 16:43:31 ON 21 JAN 96
L1            272 FILE MEDLINE
L2            256 FILE BIOSIS
L3             56 FILE CAPLUS
     TOTAL FOR ALL FILES
L4            584 S BRENNER S/AU
L5             48 FILE MEDLINE
L6             42 FILE BIOSIS
L7              8 FILE CAPLUS
     TOTAL FOR ALL FILES
L8             98 S L4 AND SEQUENC?
L9             56 DUP REM L8 (42 DUPLICATES REMOVED)
L10             0 FILE MEDLINE
L11             0 FILE BIOSIS
L12             0 FILE CAPLUS
     TOTAL FOR ALL FILES
L13             0 S L4 AND SORT###
L14            22 FILE MEDLINE
L15            23 FILE BIOSIS
L16            27 FILE CAPLUS
     TOTAL FOR ALL FILES
L17            72 S OLIGONUCLEOTIDE# (3A) TAG####
L18            36 DUP REM L17 (36 DUPLICATES REMOVED)
L19           197 FILE MEDLINE
L20           249 FILE BIOSIS
L21           167 FILE CAPLUS
     TOTAL FOR ALL FILES
L22           613 S SORT### (3A) (CDNA OR DNA OR MRNA OR POLYNUCLEOTIDE# OR
L23           326 DUP REM L22 (287 DUPLICATES REMOVED)

=> s (multiplex or parallel) (3a) sequenc?

L24           129 FILE MEDLINE
L25           175 FILE BIOSIS
L26           297 FILE CAPLUS

TOTAL FOR ALL FILES
L27           601 (MULTIPLEX OR PARALLEL) (3A) SEQUENC?

=> s l27 and (nucleic or DNA or RNA or polynucleot?)
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=> s l27 and nucleic

L28          38 FILE MEDLINE
L29           3 FILE BIOSIS
L30          23 FILE CAPLUS

TOTAL FOR ALL FILES
L31          64 L27 AND NUCLEIC

=> dup rem l31

PROCESSING COMPLETED FOR L31
L32           59 DUP REM L31 (5 DUPLICATES REMOVED)
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L18 ANSWER 15 OF 36 MEDLINE DUPLICATE 6

AU Needels M C; Jones D G; Tate E H; Heinkel G L; Kochersperger L M; Dower W J; Barrett R W; Gallop M A

TI Generation and screening of an oligonucleotide-encoded synthetic peptide library.

SO Proc Natl Acad Sci U S A, (1993 Nov 15) 90 (22) 10700-4.
Journal code: PV3. ISSN: 0027-8424.

AB We have prepared a library of approximately 10(6) different peptide sequences on small, spherical (10-microns diameter) beads by the combinatorial chemical coupling of both L- and D-amino acid building blocks. To each bead is covalently attached many copies of a single peptide sequence and, additionally, copies of a unique single-stranded oligonucleotide that codes for that peptide sequence. The ***oligonucleotide*** ***tags*** are synthesized through a parallel combinatorial procedure that effectively records the process by which the encoded peptide sequence is assembled. The collection of beads was screened for binding to a fluorescently labeled anti-peptide antibody using a fluorescence-activated cell sorting instrument. Those beads to which the antibody bound tightly were isolated by fluorescence-activated sorting, and the oligonucleotide identifiers attached to individual sorted beads were amplified by the PCR. Sequences of the amplified DNAs were determined to reveal the identity of peptide sequences that bound to the antibody with high affinity. By combining the capacity for information storage in an oligonucleotide code with the tremendous level of amplification possible through the PCR, we have devised a means for specifying the identity of each member of a vast library of molecules synthesized from both natural and unnatural chemical building blocks. In addition, we have shown that the use of flow cytometry instrumentation permits facile isolation of individual beads that bear high-affinity ligands for biological receptors.

L23 ANSWER 57 OF 326 CAPLUS COPYRIGHT 1996 ACS
IN Chetverin, Alexander B.; Kramer, Fred Russell
TI Oligonucleotide arrays and their use for sorting, isolating, sequencing, and manipulating nucleic acids
SO PCT Int. Appl., 103 pp.
CODEN: PIXXD2
AB Binary oligonucleotides having a const. nucleotide sequence adjacent to a variable nucleotide sequence are used for ***sorting*** and surveying ***nucleic*** acid strands. These oligonucleotide arrays are used for ***sorting*** mixt. of ***nucleic*** acid strands, making immobilized partial copies of nucleic acid strands, ligating strands, or introducing site directed mutations into strands. Information is obtained for detg. the sequence of a nucleic acid strand, alone or in a mixt., by generating partials of the strand and, for groups of partials having the same terminal variable oligonucleotide, sep. detg. the presence and sequence of all variable oligonucleotide. Arrays are also used to order previously sequenced nucleic acid fragments and to allocate ordered allelic fragments to chromosomal linkage groups.

=> d 57

L23 ANSWER 57 OF 326 CAPLUS COPYRIGHT 1996 ACS
AN 1993:597263 CAPLUS
DN 119:197263
TI Oligonucleotide arrays and their use for sorting, isolating, sequencing, and manipulating nucleic acids
IN Chetverin, Alexander B.; Kramer, Fred Russell
PA Public Health Research Institute of the City of New York, Inc., USA
SO PCT Int. Appl., 103 pp.
CODEN: PIXXD2
PI WO 9317126 A1 930902
DS W: AT, AU, BB, BG, BR, CA, CH, DE, DK, ES, FI, GB, HU, JP, KP, KR, LK, LU, MG, MN, MW, NL, NO, PL, RO, RU, SD, SE
RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, DE, DK, ES, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NL, PT, SE, SN, TD, TG
AI WO 93-US1552 930219
PRAI US 92-838607 920219
DT Patent
LA English

L32 ANSWER 15 OF 59 CAPLUS COPYRIGHT 1996 ACS

AU Egholm, Michael; Behrens, Carsten; Christensen, Leif; Berg, Rolf H.; Nielsen, Peter E.; Buchardt, Ole

TI Peptide ***nucleic*** acids containing adenine or guanine recognize thymine and cytosine in complementary DNA sequences

SO J. Chem. Soc., Chem. Commun. (1993), (9), 800-1
CODEN: JCCCAT; ISSN: 0022-4936

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=> d his
     (FILE 'USPAT' ENTERED AT 14:55:23 ON 21 JAN 96)
L1         54138 S SORT###
L2         17725 S #DNA OR POLYNUCLEOTIDE# OR #RNA OR NUCLEIC
L3          1006 S L1 AND L2
L4           323 S L1(P)L2
L5            61 S L1(3A)L2
L6          4224 S OLIGONUCLEOTIDE#
L7           150 S L6 (P) TAG####
L8            28 S L6 (3A) TAG####
L9            93 S (MULTIPLEX OR PARALLEL) (3A) SEQUENCING
L10           31 S L9 AND L2
L11            0 S L8 AND 5451505/PN
L12           29 S L6 (4A)TAG#### NOT L5
L13            4 S HYBRIDIZATION (3A) TAG#
L14          245 S AFFINITY (P) (OLIGONUCLEOTIDE#)
L15           40 S AFFINITY (3A) (OLIGONUCLEOTIDE#)
```

=> d 3,18,25 cit ab

3. 5,470,710, Nov. 28, 1995, Automated hybridization/imaging device for fluorescent multiplex DNA sequencing; Robert B. Weiss, et al., 435/6, 7.1, 7.5, 7.9 [IMAGE AVAILABLE]

US PAT NO: 5,470,710 [IMAGE AVAILABLE] L8: 3 of 28

ABSTRACT:
A method is disclosed for automated multiplex sequencing of DNA with an integrated automated imaging hybridization chamber system. This system comprises an hybridization chamber device for mounting a membrane containing size-fractionated multiplex sequencing reaction products, apparatus for fluid delivery to the chamber device, imaging apparatus for light delivery to the membrane and image recording of fluorescence emanating from the membrane while in the chamber device, and programmable controller apparatus for controlling operation of the system. The multiplex reaction products are hybridized with a probe, then an enzyme (such as alkaline phosphatase) is bound to a binding moiety on the probe, and a fluorogenic substrate (such as a benzothiazole derivative) is introduced into the chamber device by the fluid delivery apparatus. The enzyme converts the fluorogenic substrate into a fluorescent product which, when illuminated in the chamber device with a beam of light from the imaging apparatus, excites fluorescence of the fluorescent product to produce a pattern of hybridization. The pattern of hybridization is imaged by a CCD camera component of the imaging apparatus to obtain a series of digital signals. These signals are converted by the controller apparatus into a string of nucleotides corresponding to the nucleotide sequence an automated sequence reader. The method and apparatus are also applicable to other membrane-based applications such as colony and plaque hybridization and Southern, Northern, and Western blots.

18. 5,149,625, Sep. 22, 1992, Multiplex analysis of DNA; George M. Church, et al., 435/6, 172.3, 320.1, 810; 436/808; 935/23, 24, 78 [IMAGE AVAILABLE]

US PAT NO: 5,149,625 [IMAGE AVAILABLE] L8: 18 of 28

ABSTRACT:
This invention features vectors and a method for sequencing DNA. The method includes the steps of:
a) ligating the DNA into a vector comprising a tag sequence, the tag sequence includes at least 15 bases, wherein the tag sequence will not hybridize to the DNA under stringent hybridization conditions and is unique in the vector, to form a hybrid vector,
b) treating the hybrid vector in a plurality of vessels to produce fragments comprising the tag sequence, wherein the fragments differ in

length and terminate at a fixed known base or bases, wherein the fixed known base or bases differs in each vessel,

c) separating the fragments from each vessel according to their size,

d) hybridizing the fragments with an oligonucleotide able to hybridize specifically with the tag sequence, and

e) detecting the pattern of hybridization of the tag sequence, wherein the pattern reflects the nucleotide sequence of the DNA.

25. 4,942,124, Jul. 17, 1990, Multiplex sequencing; George M. Church, 435/6, 172.3, 803; 436/501; 935/23, 24, 29, 77, 78 [IMAGE AVAILABLE]

US PAT NO: 4,942,124 [IMAGE AVAILABLE] L8: 25 of 28

ABSTRACT:
This invention features vectors and a method for sequencing DNA. The method includes the steps of:
(a) ligating the DNA into a vector comprising a tag sequence, the tag sequence includes at least 15 bases, wherein the tag sequence will not hybridize to the DNA under stringent hybridization conditions and is unique in the vector, to form a hybrid vector,
(b) treating the hybrid vector in a plurality of vessels to produce fragments comprising the tag sequence, wherein the fragments differ in length and terminate at a fixed known base or bases, wherein the fixed known base or bases differs in each vessel,
(c) separating the fragments from each vessel according to their size,
(d) hybridizing the fragments with an oligonucleotide able to hybridize specifically with the tag sequence, and
(e) detecting the pattern of hybridization of the tag sequence, wherein the pattern reflects the nucleotide sequence of the DNA.